BIOTECHNOLOGY SYSTEMS BRANCH

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable #11/2 form:

Application Serial Number: 09

Source:

Date Processed by STIC:

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS. PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

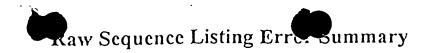
TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2Kcompliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker



ERROR DETECTED SUGGESTED CORRECTION

ALIN 1	Wrapped Nucleics	PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE The number/text at the end of each line "wrapped" down to the next line.
· 		This may occur if your file was retrieved in a word processor after creating it.
		Please adjust your right margin to .3, as this will prevent "wrapping".
2	Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line.
	•	This may occur if your file was retrieved in a word processor after creating it.
		Please adjust your right margin to .3, as this will prevent "wrapping".
3	Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.
4	Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
5	Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
		Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
6	Variable Length	Sequence(s) contain n's or Xaa's which represented more than one residue.
		As per the rules, each n or Xaa can only represent a single residue.
		Please present the maximum number of each residue having variable length and
		indicate in the (ix) feature section that some may be missing.
7	Patentin ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
	•	sequence(s) Normally, Patentin would automatically generate this section from the
		previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
		to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
		sections for Artificial or Unknown sequences.
8	Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X:
	(012)	(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
		This sequence is intentionally skipped
•		
		Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
9	Skipped Sequences	Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
	(NEW RULES)	<210> sequence id number
		\$400> sequence id number 000
10	Use of n's or Xaa's	Use of n's and/or Xaa's have been detected in the Sequence Listing.
	(NEW RULES)	Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
		In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
11	Use of <213>Organism	Sequence(s) are missing this mandatory field or its response.
	(NEW RULES)	
12	Use of <220>Feature	Sequence(s) are missing the <220>Feature and associated headings.
·	(NEW RULES)	Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
		Please explain source of genetic material in <220> to <223> section.
		(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
13	Patentin ver. 2.0 "bug"	Please do not use "Copy to Disk" function of Patentln version 2.0. This causes a corrupted
		file reguling in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).

Instead, please use "File Manager" or any other means to copy file to floppy disk.

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Corrected Diskette Needed

| Corrected Diskette Needed | Construct | Construct

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about is a sample of submitted file. Major format errors.

Sample of submitted file. Major format errors.

Please see cover sheet, and contact Robert Wax at 703-306-4/19, for assistance.

responses are: Unknown,
Artificial Sequence, or
Scientific name (benus/species)
(one of the three). See
1.823 of new Sequence Rules
and Fren 12 (circled portion)
on Euro Summany Steet.

Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.